RAW SEQUENCE LISTING
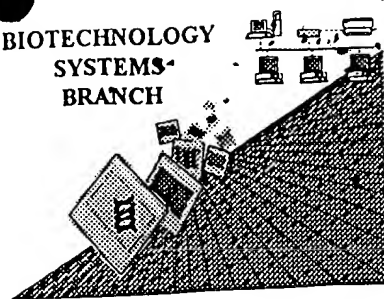## ERROR REPORT

BIOTECHNOLOGY
SYSTEMS-
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___09/974619___

Source: ___OIPE___

Date Processed by STIC: ___10/30/01___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/974619

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P1

1_____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length.

Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)_____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
(OLD RULES)

Sequence(s)_____missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
(NEW RULES)

Sequence(s)_____missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10_____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence

11_____Use of <220>

Sequence(s)_____missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represe any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 10/30/2001
PATENT APPLICATION: US/09/974,619   TIME: 11:27:52

Input Set : A:\1340-1-034N.ST25.txt
Output Set: N:\CRF3\10302001\I974619.raw

```
      3 <110> APPLICANT: Schuetz, Erin
      4        Zhang, Jiong
      5        Assem, Mahfoud
      7 <120> TITLE OF INVENTION: GENOTYPING ASSAY TO PREDICT CYP3A5 PHENOTYPE
      9 <130> FILE REFERENCE: 1340-1-034N
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/974,619
     12 <141> CURRENT FILING DATE: 2001-10-10
     14 <150> PRIOR APPLICATION NUMBER: 60/279,915
     15 <151> PRIOR FILING DATE: 2001-03-29
     17 <160> NUMBER OF SEQ ID NOS: 36
     19 <170> SOFTWARE: PatentIn version 3.1
     21 <210> SEQ ID NO: 1
     22 <211> LENGTH: 23
     23 <212> TYPE: DNA
C--> 24 <213> ORGANISM: Artificial
W--> 26 <220> FEATURE:
W--> 26 <223> OTHER INFORMATION:
     26 <400> SEQUENCE: 1
     27 tgggatgaat ttcaagtatt ttg
     30 <210> SEQ ID NO: 2
     31 <211> LENGTH: 20
     32 <212> TYPE: DNA
C--> 33 <213> ORGANISM: Artificial
W--> 35 <220> FEATURE:
W--> 35 <223> OTHER INFORMATION:
     35 <400> SEQUENCE: 2
     36 aggtttccat ggccaagtct
     39 <210> SEQ ID NO: 3
     40 <211> LENGTH: 20
     41 <212> TYPE: DNA
C--> 42 <213> ORGANISM: Artificial
W--> 44 <220> FEATURE:
W--> 44 <223> OTHER INFORMATION:
     44 <400> SEQUENCE: 3
     45 ccgatcagaa taaggcattg
     48 <210> SEQ ID NO: 4
     49 <211> LENGTH: 20
     50 <212> TYPE: DNA
C--> 51 <213> ORGANISM: Artificial
W--> 53 <220> FEATURE:
W--> 53 <223> OTHER INFORMATION:
     53 <400> SEQUENCE: 4
     54 gattcacctg gggtcaacac
     57 <210> SEQ ID NO: 5
     58 <211> LENGTH: 23
     59 <212> TYPE: DNA
C--> 60 <213> ORGANISM: Artificial
```

Errored: A field 2133 response of "Artificial" requires a mandatory response in field 223.

FYI: "Artificial Sequence" is the preferred response on field 213.

20

20

20

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

```
        170 <400> SEQUENCE: 17                                          22
        171 gcctaaagac cttcgatttg tg
        174 <210> SEQ ID NO: 18
        175 <211> LENGTH: 22
        176 <212> TYPE: DNA
C--> 177 <213> ORGANISM: Artificial
W--> 179 <220> FEATURE:
W--> 179 <223> OTHER INFORMATION:
        179 <400> SEQUENCE: 18                                          22
        180 cattccttac cccagttttt ga
        183 <210> SEQ ID NO: 19
        184 <211> LENGTH: 24
        185 <212> TYPE: DNA
C--> 186 <213> ORGANISM: Artificial
W--> 188 <220> FEATURE:
W--> 188 <223> OTHER INFORMATION:
        188 <400> SEQUENCE: 19                                          24
        189 agtcctctca agtctaatag caac
        192 <210> SEQ ID NO: 20
        193 <211> LENGTH: 23
        194 <212> TYPE: DNA
C--> 195 <213> ORGANISM: Artificial
W--> 197 <220> FEATURE:
W--> 197 <223> OTHER INFORMATION:
        197 <400> SEQUENCE: 20                                          23
        198 gaaggacagc atagatcctt aca
        201 <210> SEQ ID NO: 21
        202 <211> LENGTH: 22
        203 <212> TYPE: DNA
C--> 204 <213> ORGANISM: Artificial
W--> 206 <220> FEATURE:
W--> 206 <223> OTHER INFORMATION:
        206 <400> SEQUENCE: 21                                          22
        207 cagggtctct ggaaatttga ca
        210 <210> SEQ ID NO: 22
        211 <211> LENGTH: 22
        212 <212> TYPE: DNA
C--> 213 <213> ORGANISM: Artificial
W--> 215 <220> FEATURE:
W--> 215 <223> OTHER INFORMATION:
        215 <400> SEQUENCE: 22                                          22
        216 tcattctcca cttagggttc ca
        219 <210> SEQ ID NO: 23
        220 <211> LENGTH: 22
        221 <212> TYPE: DNA
C--> 222 <213> ORGANISM: Artificial
W--> 224 <220> FEATURE:
W--> 224 <223> OTHER INFORMATION:
        224 <400> SEQUENCE: 23
```

```
      225 cagcatggat gtgattactg gc                                    22
      228 <210> SEQ ID NO: 24
      229 <211> LENGTH: 21
      230 <212> TYPE: DNA
C--> 231 <213> ORGANISM: Artificial
W--> 233 <220> FEATURE:
W--> 233 <223> OTHER INFORMATION:
      233 <400> SEQUENCE: 24
      234 cctgccttca atttttcact g                                     21
      237 <210> SEQ ID NO: 25
      238 <211> LENGTH: 20
      239 <212> TYPE: DNA
C--> 240 <213> ORGANISM: Artificial
W--> 242 <220> FEATURE:
W--> 242 <223> OTHER INFORMATION:
      242 <400> SEQUENCE: 25
      243 gcaatgtagg aaggagggct                                       20
      246 <210> SEQ ID NO: 26
      247 <211> LENGTH: 20
      248 <212> TYPE: DNA
C--> 249 <213> ORGANISM: Artificial
W--> 251 <220> FEATURE:
W--> 251 <223> OTHER INFORMATION:
      251 <400> SEQUENCE: 26
      252 taatattctt tttgataatg                                       20
      255 <210> SEQ ID NO: 27
      256 <211> LENGTH: 22
      257 <212> TYPE: DNA
C--> 258 <213> ORGANISM: Artificial
W--> 260 <220> FEATURE:
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      261 cattctttca ctagcactgt tc                                    22
      264 <210> SEQ ID NO: 28
      265 <211> LENGTH: 20
      266 <212> TYPE: DNA
C--> 267 <213> ORGANISM: Artificial
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      270 caacaaaaac cggcaaactg                                       20
      273 <210> SEQ ID NO: 29
      274 <211> LENGTH: 20
      275 <212> TYPE: DNA
C--> 276 <213> ORGANISM: Artificial
W--> 278 <220> FEATURE:
W--> 278 <223> OTHER INFORMATION:
      278 <400> SEQUENCE: 29
      279 aggattttca gacttaacac                                       20
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/974,619

DATE: 10/30/2001
TIME: 11:27:54

Input Set : A:\1340-1-034N.ST25.txt
Output Set: N:\CRF3\10302001\I974619.raw

```
L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:24 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:26 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:26 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:33 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:35 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:35 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:42 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:44 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:44 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:51 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:53 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:53 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:60 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:62 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:62 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:69 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
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L:71 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:78 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:80 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:80 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:87 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:89 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:89 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:96 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:98 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:98 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:105 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:107 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:107 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:114 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
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L:132 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
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L:134 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:143 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:152 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:159 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:161 M:258 W: Mandatory Feature missing, <220> FEATURE:
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VERIFICATION SUMMARY
DATE: 10/30/2001
PATENT APPLICATION: US/09/974,619
TIME: 11:27:54

Input Set : A:\1340-1-034N.ST25.txt
Output Set: N:\CRF3\10302001\I974619.raw

```
L:161 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:170 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:179 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:186 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:188 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:188 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:195 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
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L:197 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:204 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
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L:206 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:213 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:215 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:215 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:222 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:224 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:224 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:231 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:233 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:233 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:240 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
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L:242 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:249 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:258 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:267 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:276 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:285 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:294 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:303 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:312 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:321 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:330 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35
L:339 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36
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